We claim:

1. A system for predicting alternative splicing transcripts using DNA chip expression data, the system comprising:

an expression profiling subsystem configured to provide DNA chip expression data;

a processor, coupled to the expression profiling subsystem configured to analyze the DNA chip expression data,

a network interface, coupled to both the processor and the expression profiling subsystem that is configured to provide access to data related to gene profiling.

2. The system of claim 1, wherein the network interface is coupled to a network that is coupled to a host server that stored the data related to gene profiling.

3. The system of claim 1, further comprising a memory coupled to the processor configured to store operating instructions for the processor.

4. The system of claim 3, further comprising a user interface coupled to the processor and the network interface, the user interface being configured to provide the capability of interacting with software programs stored in the memory and used by the processor .

5. The system of claim 4, wherein the user interface is also configured to provide access to data related to gene profiling via the network interface, which is coupled to a network that is coupled to a host server that stores the data related to gene profiling.

6. The system of claim 1, further comprising a controller coupled to the processor and the network interface and that controls operation of the processor and the network interface and cooperation of the processor, network interface and expression profiling subsystem.

7. The system of claim 1, wherein the expression profiling subsystem comprises at least one high density, oligonucleotide probe micro-array.

8. The system of claim 7, wherein the micro-array includes a set of oligonucleotide probes that generate, from control and treatment sets of cell-derived samples, respective sets of gene expression data representing a direction and a magnitude of regulation of nucleic acid sequences.

9. The system of claim 1, wherein the expression profiling subsystem obtains the DNA chip expression data and stores that data in an organized fashion in a host server coupled to the processor via the network interface.

10. The system of claim 9, further comprising a controller coupled to the processor and the network interface and that controls operation of the processor and the network interface and cooperation of the processor, network interface and expression profiling subsystem, wherein the controller controls the cooperation between the processor and the host server.

11. The system of claim 10, wherein the host server is provided with an analysis application for performing analysis associated with expression profiling and managing the data acquired from the DNA chip expression data.

12. A method for predicting alternative splicing transcripts using DNA chip expression data, the method comprising:

performing test sample preparation and hybridization for a set of tissue samples during which hybridization reactions of the set of tissue samples are scanned;

preprocessing data resulting from the scanned hybridization reactions; and

performing a first splice variant prediction to produce first splice variant prediction data.

13. The method of claim 12, further comprising performing a second splice variant prediction to produce second splice-variant prediction data.

14. The method of claim 12, wherein sample preparation and hybridization comprises:

extracting total RNA from the set of tissue samples;

preparing double-stranded cDNA from the extracted total RNA;

performing phenol-chloroform extraction and ethanol precipitation on the double-stranded cDNA to produce a cDNA reaction;

using one-half of the cDNA reaction as a template in an in vitro transcription reaction to produce cRNA;

purifying and quantifying the cRNA;

randomly fragmenting the cRNA;

hybridizing the randomly fragmented cRNA; and

scanning the results of hybridization.

15. The method of claim 12, wherein preprocessing data resulting from the scanned hybridization reaction comprises:

extracting raw signal intensity readings of each probe on the DNA chip in the data resulting from the scanned hybridization reaction;

normalizing the extracted raw signal intensity readings by removing noise resulting from background hybridization from the extracted raw signal intensity readings;

performing global scaling on the normalized raw signal intensity readings;

generating a normalized difference table by subtracting each mismatch signal from its corresponding perfect match signal within the normalized and scaled intensity readings; and

generating a normalized ratio table by dividing the perfect match and mismatch signals of each probe pair within the normalized and scaled intensity readings.

16. The method of claim 12, wherein performing a first splice variant prediction to produce first splice variant prediction data comprises:

combining a normalized difference table and a normalized ratio table produced by the preprocessing step to generate a signal strength table;

filtering out data in the signal strength table that corresponds to uninformative probes using at least one cut-off threshold;

calculating the average difference of each probe set in each tissue sample;
calculating the average difference of each probe across different tissue samples;
calculating tissue-specific relative signal strength data by normalizing the expression level across tissues in the normalized and thresholded signal strength data; and
convert the tissue-specific relative signal strength data to a final log ratio.

17. The method of claim 13, wherein performing a second splice variant prediction to produce second splice-variant prediction data comprises sorting splice variant prediction data generated by performing a first splice variant prediction to prioritize the data.